

# SEQUENCE LISTING

<110> Allen, Keith D.  
Leviten, Michael W.

<120> TRANSGENIC MICE CONTAINING CASH GENE  
DISRUPTIONS

<130> R-714

<150> US 60/254,902

<151> 2000-12-11

<160> 4

<170> FastSEQ for Windows Version 4.0

<210> 1

<211> 2770

<212> DNA

<213> Mus musculus

<400> 1

```

ggcttctcgt ggttcccaga gccctgctta atggatggag actggacgag aacctggctg 60
ctgtgggttct gaacatggcc cagagccctg tgtctgccga ggctattcac caggtggaag 120
agtgtcttga tgaagacgag aaggagatga tgctcttcct gtgtagagat gtgactgaga 180
acctggctgc acctaacgtc agggacctcc tggatagctt aagttagaga ggccagctct 240
cttttgctac cttggctgaa ttgctctaca gagttaggag gtttgacctt ctcaagagga 300
tcttgaagac agacaaagca accgtggagg accacctgag cagaaacctt cacctgggtt 360
ctgattatag ggtcctgctg atggagattg gtgagagctt agatcagaac gatgtatcct 420
ccttagtttt ccttacaagg attacaaggg attacacagg cagaggcaag atagccaagg 480
acaagagttt cttggatctg gtgattgaat tggagaaact gaatctaatt gcttcagacc 540
aattgaattt gttagaaaaa tgctgaaga acatccacag aatagacttg aacacaaaga 600
tccagaagta caccagctcc agccaaggag caagatcaaa tatgaatact ctccaggctt 660
cgctcccaaa attgagtatc aagtataact caaggctcca gaatgggcca agtaaagagc 720
caagatttgt ggaataccgt gacagtcaaa gaacactggt gaagacatcc atccaggaat 780
caggagcttt tttacctccg cacatccgtg aagagactta caggatgcag agcaagcccc 840
taggaatctg cttgatcatt gattgtattg gcaacgacac aaaatatctt caagagacct 900
tcacttccct gggctatcat atccagcttt tcttgtttcc caagtcacat gacataacct 960
agattgttcg ccgatatgca agtatggccc aacatcaaga ctatgacagc tttgcatgtg 1020
ttctgggtgag cctaggaggc tcccaaagca tgatgggcag agatcaagtt cactcagggg 1080
tctccttgga tcatgtcaag aacatgttca cgggggacac gtgcccttct ctcaagggga 1140
agccaaagct cttttttatt cagaactatg agtcgttagg tagccagttg gaagatagca 1200
gcctggagggt agatgggcca tcaataaaaa atgtggactc taagcccctg caaccagac 1260
actgcacaac tcaccagaa gctgatatct tttggagcct gtgcacagca gacgtatctc 1320
acttgagaa gccctccagc tcatcctctg tgtatctgca gaagctctcc cagcagctga 1380
agcaaggcag gagacgcca ctctgggacc tccacgttga actcatggac aaagtgtatg 1440
cgtggaacag tgggtgttcg tctaaggaga aatacagcct cagcctgcag cacactctga 1500
ggaagaaact catcctggct cctacgtgag aacccagac cgttggtgtt cttggtatat 1560
catccagggg ggcggcttgg agcagagctt ggcgggttac gctgcttctg gctgcttctg 1620
gctctgccgt gagtcttggc ctagggttct cctgtgcaca ggcagtagcc gtaaccctgt 1680
gcctgggaaa cgtctcactc ccgcccgcgt gcctttacct ctctaaactt ccctacttac 1740
attccttagt cggatgtttt gccagagtgt ggagaacagt aagacataaa cctattgttt 1800
gtttgttttt ttggggggga ggttatctac caagttatac caagttattg tatgggtgta 1860
tagtgtatag tggttcaaga ttctgaatgt aacttgagac ttacctgagt ttgtcatgag 1920
actgggtaaa ttgtttctat ggcacatcta atcatttaac aagtaattac ctcatatagt 1980
acctattgct tcaggacttt cacattggcc accaatttct gtgaccagc tccacattta 2040
tattctcttt cggcaaaacc aaatttctat atgtctgttt aatatctaca gtctaagtgt 2100
ttgtaagaca tctagatagg aaaaatagtt acccatgagc acaggagggc tggcctgacc 2160
ctcaccagct gtgcagtggc ttcggtgaaa ggagaatgag ccctactcct tgaaagggtg 2220

```

```

tagtgcttgg gagagcagtc tgtaccttgc ctgggcagca cagtagagcc agccccaaga 2280
acacaacagt gagtggggga gcttgccctg gttggctcag gatcaggaaa caggagggat 2340
gaccaacttg gggctttgag gtggcccacc ccagcatcca tatcatctgt gaactgccag 2400
agcctgtgaa ggggcgggtc ctgtagaact aaggctgcag gatctccatg acacagggca 2460
acaacagggt atctgagaag ggtccccgtg aggggtccagt atttatagtg caccagaagc 2520
cagaggcctc ggatcagaca atgaccatt gcactgagta aagatgtaag tgaatgagtg 2580
aagatgtgtg ggcacacgga aatactgagg gacacacaca agcttttatg gagatgtttg 2640
tttgtttgtt tgtttgtttt ttgtttcttt ggcaggaaca gattgcaagg gcagagagta 2700
gataaggaag ctggagacat gagtgggggt ggggtgcatga tatagaattc acaaagaaaa 2760
aaaaaaaaa 2770

```

<210> 2  
 <211> 484  
 <212> PRT  
 <213> Mus musculus

<400> 2

Met	Ala	Gln	Ser	Pro	Val	Ser	Ala	Glu	Val	Ile	His	Gln	Val	Glu	Glu
1				5					10					15	
Cys	Leu	Asp	Glu	Asp	Glu	Lys	Glu	Met	Met	Leu	Phe	Leu	Cys	Arg	Asp
		20						25					30		
Val	Thr	Glu	Asn	Leu	Ala	Ala	Pro	Asn	Val	Arg	Asp	Leu	Leu	Asp	Ser
		35					40					45			
Leu	Ser	Glu	Arg	Gly	Gln	Leu	Ser	Phe	Ala	Thr	Leu	Ala	Glu	Leu	Leu
	50				55					60					
Tyr	Arg	Val	Arg	Arg	Phe	Asp	Leu	Leu	Lys	Arg	Ile	Leu	Lys	Thr	Asp
65					70					75				80	
Lys	Ala	Thr	Val	Glu	Asp	His	Leu	Arg	Arg	Asn	Pro	His	Leu	Val	Ser
			85						90					95	
Asp	Tyr	Arg	Val	Leu	Leu	Met	Glu	Ile	Gly	Glu	Ser	Leu	Asp	Gln	Asn
			100					105					110		
Asp	Val	Ser	Ser	Leu	Val	Phe	Leu	Thr	Arg	Ile	Thr	Arg	Asp	Tyr	Thr
		115					120					125			
Gly	Arg	Gly	Lys	Ile	Ala	Lys	Asp	Lys	Ser	Phe	Leu	Asp	Leu	Val	Ile
	130				135						140				
Glu	Leu	Glu	Lys	Leu	Asn	Leu	Ile	Ala	Ser	Asp	Gln	Leu	Asn	Leu	Leu
145					150					155					160
Glu	Lys	Cys	Leu	Lys	Asn	Ile	His	Arg	Ile	Asp	Leu	Asn	Thr	Lys	Ile
			165						170					175	
Gln	Lys	Tyr	Thr	Gln	Ser	Ser	Gln	Gly	Ala	Arg	Ser	Asn	Met	Asn	Thr
		180						185					190		
Leu	Gln	Ala	Ser	Leu	Pro	Lys	Leu	Ser	Ile	Lys	Tyr	Asn	Ser	Arg	Leu
		195					200					205			
Gln	Asn	Gly	Arg	Ser	Lys	Glu	Pro	Arg	Phe	Val	Glu	Tyr	Arg	Asp	Ser
	210				215						220				
Gln	Arg	Thr	Leu	Val	Lys	Thr	Ser	Ile	Gln	Glu	Ser	Gly	Ala	Phe	Leu
225					230					235				240	
Pro	Pro	His	Ile	Arg	Glu	Glu	Thr	Tyr	Arg	Met	Gln	Ser	Lys	Pro	Leu
			245						250					255	
Gly	Ile	Cys	Leu	Ile	Ile	Asp	Cys	Ile	Gly	Asn	Asp	Thr	Lys	Tyr	Leu
		260						265					270		
Gln	Glu	Thr	Phe	Thr	Ser	Leu	Gly	Tyr	His	Ile	Gln	Leu	Phe	Leu	Phe
		275					280					285			
Pro	Lys	Ser	His	Asp	Ile	Thr	Gln	Ile	Val	Arg	Arg	Tyr	Ala	Ser	Met
	290					295					300				
Ala	Gln	His	Gln	Asp	Tyr	Asp	Ser	Phe	Ala	Cys	Val	Leu	Val	Ser	Leu
305					310					315					320
Gly	Gly	Ser	Gln	Ser	Met	Met	Gly	Arg	Asp	Gln	Val	His	Ser	Gly	Phe
			325						330					335	
Ser	Leu	Asp	His	Val	Lys	Asn	Met	Phe	Thr	Gly	Asp	Thr	Cys	Pro	Ser
			340					345					350		

Leu	Arg	Gly	Lys	Pro	Lys	Leu	Phe	Phe	Ile	Gln	Asn	Tyr	Glu	Ser	Leu
		355					360					365			
Gly	Ser	Gln	Leu	Glu	Asp	Ser	Ser	Leu	Glu	Val	Asp	Gly	Pro	Ser	Ile
	370					375					380				
Lys	Asn	Val	Asp	Ser	Lys	Pro	Leu	Gln	Pro	Arg	His	Cys	Thr	Thr	His
385					390					395					400
Pro	Glu	Ala	Asp	Ile	Phe	Trp	Ser	Leu	Cys	Thr	Ala	Asp	Val	Ser	His
			405						410					415	
Leu	Glu	Lys	Pro	Ser	Ser	Ser	Ser	Ser	Val	Tyr	Leu	Gln	Lys	Leu	Ser
		420						425					430		
Gln	Gln	Leu	Lys	Gln	Gly	Arg	Arg	Arg	Pro	Leu	Val	Asp	Leu	His	Val
		435					440					445			
Glu	Leu	Met	Asp	Lys	Val	Tyr	Ala	Trp	Asn	Ser	Gly	Val	Ser	Ser	Lys
	450					455					460				
Glu	Lys	Tyr	Ser	Leu	Ser	Leu	Gln	His	Thr	Leu	Arg	Lys	Lys	Leu	Ile
465					470					475					480
Leu	Ala	Pro	Thr												

<210> 3  
 <211> 200  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting Vector

<400> 3  
 cctgtgcttt gactctcaag cctaagtgtt ttgataagag gattctcttt caccacagag 60  
 tgtctctatt gcaagaactc tgagagaaat gaagagagtc ctcagcaatg atgttggctt 120  
 ctggtggttc ccagagccct gcttaatgga tggagactgg acgagaacct ggctgctgtg 180  
 gttctgaaca tggcccagag 200

<210> 4  
 <211> 200  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Targeting Vector

<400> 4  
 cttggctgaa ttgctctaca gagtgaggcg gtttgacctt ctcaagagga tcttgaagac 60  
 agacaaagca accgtggagg accacctgcg cagaaaccct cacctgggtt ctgattatag 120  
 gtaagtcac ccctggggga ggggagaggg agtctagatg gttagggcag tgagaagacc 180  
 ccattgcttc ctcttctctc 200